

~~OAC 3/27/01 0500 OIRE~~Serial Number: 09/733,685CRF Processing Date: 12/21/2000

Edited by:

Verified by:

(STIC Staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was wrapped down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

Other:

Segr 22-23 - inserted hard returns

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,685 DATE: 12/21/2000
 TIME: 10:14:24
 Input Set : A:\seq-list.txt
 Output Set: N:\CRF3\12212000\I733685.raw

Does Not Comp'y
 Corrected Diskette Needed

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3 <110> APPLICANT: Cade, Rebecca M
4      Dietrich, Robert A
6 <120> TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
7      SAR GENE EXPRESSION IN PLANTS
9 <130> FILE REFERENCE: A-31089A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/733,685
C--> 12 <141> CURRENT FILING DATE: 2000-12-08
14 <150> PRIOR APPLICATION NUMBER: 60/171,008
15 <151> PRIOR FILING DATE: 1999-12-15
17 <150> PRIOR APPLICATION NUMBER: 60/175,519
18 <151> PRIOR FILING DATE: 2000-01-11
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 509
26 <212> TYPE: DNA
27 <213> ORGANISM: Arabidopsis thaliana
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31 <222> LOCATION: (68)..(433)
32 <223> OTHER INFORMATION: gene product NIL6
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (142)..(147)
37 <223> OTHER INFORMATION: SalI site
39 <220> FEATURE:
40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (344)..(349)
42 <223> OTHER INFORMATION: EcoRI site
44 <400> SEQUENCE: 1
45 aaaaatcugca aataaacttt tcttgactaa gcttaaacga cggccgttaac attttcttc 60
47 ggctaacatq aac aac tct ttg aag aaa gaa gaa cgc gta qaa gaa gat 109
48      Met Asn Asn Ser Ileu Lys Lys Glu Glu Arg Val Glu Glu Asp
49      1           5           10
51 aac gga aaa tct gac ggt aac aga ggg aaa ccg tct acy gaa gtt gtt 157
52 Asn Gly Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val
53 15          20          25          30
55 cgg acg gta acy gag gaa gag gtg gat gag ttt ttc aag ata tta cgg 205
56 Arg Thr Val Thr Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg
57 35          40          45
59 aga qta cac gtg qcq aca cga acg qtt gcq aaa gtt aac ggc gqt gtt 253
60 Arg Val His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Val
61 50          55          60
63 gct gag gga gag tta ccg tct aag aag agg aaa ccg aqt cag aat ctt 301
64 Ala Glu Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gin Asn Leu
65 65          70          75
67 ggg ttg aga aac tct ttg gat tgt aac ggc gtt cga gac gga gaa ttc 349

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Input Set : A:\seq-list.txt
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68 Gly Leu Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe
69 80 85 90
71 qat qaq att aat cqq qtc ggg tta caq ggt ttg gat ctq aac 397
72 Asp Glu Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn
73 95 100 105 110
75 tgt aaa ccg gaa cca gag agc gtt agt tta tgc ttg tagacttgta 443
76 Cys Lys Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
77 115 120
79 gtccttcatg ttttccctt tcttacuata atcaattttt tttaactac aatacttttg 503
81 aaaaaa 509
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85 <211> LENGTH: 122
86 <212> TYPE: PRT
87 <213> ORGANISM: Arabidopsis thaliana
89 <400> SEQUENCE: 2
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91 1 5 10 15
93 Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val Arg Thr
94 20 25 30
96 Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg Arg Val
97 35 40 45
99 His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val Ala Glu
100 50 55 60
102 Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu Gly Leu
103 65 70 75 80
105 Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe Asp Glu
106 85 90 95
108 Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn Cys Lys
109 100 105 110
111 Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
112 115 120
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119 <213> ORGANISM: Arabidopsis thaliana
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123 <222> LOCATION: (365)..(374)
124 <223> OTHER INFORMATION: TCAL motif
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (426)..(435)
129 <223> OTHER INFORMATION: TCAL motif
131 <220> FEATURE:
132 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (609)..(614)
134 <223> OTHER INFORMATION: MYCATR22 element
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature

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Input Set : A:\seq-list.txt
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138 <222> LOCATION: (646)..(665)
139 <223> OTHER INFORMATION: CAMV AS1 salicylic acid response element
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (707)..(712)
144 <223> OTHER INFORMATION: L BOX
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (757)..(762)
149 <223> OTHER INFORMATION: HEXAMERAT 4 element
151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: (863)..(1228)
154 <223> OTHER INFORMATION: NT16 genomic coding region
156 <400> SEQUENCE: 3
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158 catgacaaaat attaatatat caqgtttaat aacatgtttt qltcttaaaa tacatgcatt 120
159 ttaaaatcag acatttgtt ltaaatcaaa tctaactct tatatacacaq cqacatlgac 180
160 gaaaaatca qgtaaaaaqa gaaaataaaq aatqugagat aqaqagattt ctatqgaaa 240
161 aqaaaqagag aacalgttaq tgaacaaat aaaaqagatat qatqatalat ttatqagaq 300
162 qtqgtqaqa ttatftttagg aqaaqqqagaq aqaaaatagaa aaaaqaaaatq acatqgtgaa 360
163 tctgaagaq atqaaatgtg itaaagatca agaagaaaaq aqaactccat ggctaaagtc 420
164 tcgtaaagaa gatgaaaaaq aaacaaaaga aqqaagaaga aagagaaaagg ctaaaataqa 480
165 ctaactatcg cc当地atc tctgtccgac aataactatc tggtccaagg ttatlttgta 540
166 tattcttttq aagtcaaaaq ttatftteta cataactct aaaaatataq ccqataccaa 600
167 ttttccaca catggactic ct当地tcca aagtcaata aagtgtgacg tcatgtact 660
168 taegctttaa aacatcgcat gatgtatgtca ttatcataa ttcacccgtt ccaattttat 720
169 tagttgttga caatacgac cgtctaaatggtt ccacacccgac ggctataaga gtttattat 780
170 aaattttagc aaaataaaat caqcaaataa tt当地tcttg actaaqctta aacgacgcgc 840
171 ttaacatattt ct当地tgcata acatgaacaa ct当地ttaag aagaagaac gctgtqaaga 900
172 agataacqqa aaatctgacg qtaacqqaqg qaaaccqctcg acqqaagtgg ttcqgacqgt 960
173 aacqgqgaa gqgqtggatq agtattttaaq qatattacqg aqagtacacq tggcqacacq 1020
174 aacggttgcg aaqgttaeq ggggttgc tggqggagag ttaccygteta aqaaagqgaa 1080
175 acqgagtcac aatcttgggt tgagaaaactc gtggattgt aacqgcttc gqagacqgqaa 1140
176 attcgatgat attaactcggg tggqgttaca gggtttgggt tggatctga actgtadacc 1200
177 ggaaccqac agcgtttagt ttcgttgcg qatattgtt ctttcatgtt ttcccttc 1260
178 ttacaataat caatttttt ttaactacaa tactttgaa aaaaatqgtt aaaaqaaat 1320
179 attaacaatgt tatccaaattt tcaatgttca qatattttt tataatgtca aqaaagaaat 1380
180 tatataatttq caaaaactaca agtcaaacaq aqgttatttia aqgttqgtt qatqgttca 1440
181 aacataaaattt ttactaaaat caatgtttt aaaaqgttqgtt qatqgttca aqaaagaaat 1500
182 ggcccttqcc tggcccgatq agtaatatttq caqgttqgtt atqgttqgtt qatqgttca 1560
183 ccaaaaadaag aqcgccgatt qccqgttqgg tgggttggg actttggattt qggatttqgtt 1620
184 catggtttat ctatataatgt ctqccggactt qttggacgacg cgttqgttct ttttctctg 1680
185 ttacqactt acqaaacat 1700
188 <210> SEQ ID NO: 4
189 <211> LENGTH: 608
190 <212> TYPE: DNA
191 <213> ORGANISM: Solanum tuberosum
193 <220> FEATURE:

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194 <221> NAME/KEY: CDS
195 <222> LOCATION: (124)..(438)
197 <400> SEQUENCE: 4
198 caggtaatac acacagaaaa catgtacata acaqatcgaa tacacattat attatattaa 60
200 tgagagaata aagagaagta attgcactag cagtattgac uattaatcg ctgcggct 120
202 tga atg cta ctt atq gac gga gaa aag aag agg aag aca gca atc 168
203 Met Leu Ile Met Asp Gly Lys Lys Arg Thr Ala Ile
204      1           5           10          15
206 ggc gcc qqa qat cqg agt aag qat qaa gta gaa gct act gtg aag gag 216
207 Gly Ala Gly Asp Arg Ser Lys Asp Glu Val Ala Thr Val Lys Glu
208           20          25          30
210 qaq gag ccq ccq tca gag qcq qaa gtt qac gag ttc ttc qcq atc tta 264
211 Glu Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu
212           35          40          45
214 cgg agg alq cat qtg qcq qtg aad tat ctc caq aqa aat gct cag att 312
215 Arg Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile
216           50          55          60
218 cgg cgg qaa aac ctt aac qca tcg ccq gcc ggt gct aac ggt gtc qca 360
219 Arg Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala
220           65          70          75
222 gct qja cgg aag aqa gaa cgg qga atc qtg aqa aaa ggt gat ttg gac 408
223 Ala Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp
224           80          85          90          95
226 ctc aac act ctg ccg qac gac ggc qga gac taa ttaacgcagt ttaaggcatag 458
227 Leu Asn Thr Leu Pro Asp Gly Gly Asp
W--> 228           100          105
230 gtttaattaca taaatgcacc ctttaattatac attagattttt aaqattgtatc tqctgtacag 518
232 atttaattatc taaaggcctt ttttttatatac atttcctcgq tauacggttt gctcttttg 578
234 attttcttta ataaatttaa tttttttatc 608
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 104
239 <212> TYPE: PRT
240 <213> ORGANISM: Solanum tuberosum
242 <400> SEQUENCE: 5
243 Met Leu Leu Met Asp Gly Glu Lys Arg Lys Arg Thr Ala Ile Gly
244      1           5           10          15
245 Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu Glu
246           20          25          30
247 Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu Arg
248           35          40          45
249 Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Arg
250           50          55          60
251 Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala Ala
252           65          70          75          80
253 Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp Leu
254           85          90          95
255 Asn Thr Leu Pro Asp Gly Gly Asp
256           100
260 <210> SEQ ID NO: 6

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Input Set : A:\seq-list.txt
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261 <211> LENGTH: 349
262 <212> TYPE: DNA
263 <213> ORGANISM: Lycopersicon esculentum
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (3)..(233)
269 <400> SEQUENCE: 6
270 ct tcg qag qga gag qtg gat qag ttt ttc gca att tta cgg agg atg 47
271 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met
272 1 5 10 15
273 cac atg gcc gta aaa tat ctt cag aqa aac gct cag att cag ccc qaa 95
274 His Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Glu Pro Glu
275 20 25 30
276 aac gtt aac gct cac ggc agc aag tta acc gca tcg cgg gcc qgt qtt 143
277 Asn Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val
278 35 40 45
279 aac gga qat gca act gga cag aaq aqa qaa cgg qga atc qtg aga aaa 191
280 Asn Gly Asp Ala Thr Gly Gin Lys Arg Glu Arg Gly Ile Val Arg Lys
281 50 55 60
282 qgt qat ttq gac ctc aac act ttq cgg qac tgc qga qac taa 233
283 Gly Asp Leu Asp Leu Asn Thr Ile Pro Asp Cys Gly Asp
284 65 70 75
285 cgcaqtttaa qcataaggta attacagaaa tgcaccttta attatcgtag attcttaaga 293
286 ttqatctgtc qlacaaattha altaaatgaa gcctttttt atatataaaa aaaaaaa 349
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 76
289 <212> TYPE: PRT
290 <213> ORGANISM: Lycopersicon esculentum
291 <400> SEQUENCE: 7
292 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met His
293 1 5 10 15
294 Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Glu Pro Glu Asn
295 20 25 30
296 Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val Asn
297 35 40 45
298 Gly Asp Ala Thr Gly Gin Lys Arg Glu Arg Gly Ile Val Arg Lys Gly
299 50 55 60
300 Asp Leu Asp Leu Asn Thr Ile Pro Asp Cys Gly Asp
301 65 70 75
302 <210> SEQ ID NO: 8
303 <211> LENGTH: 75
304 <212> TYPE: PRT
305 <213> ORGANISM: Glycine max
306 <400> SEQUENCE: 8
307 Met Glu Val Glu Lys Arg Lys Asn Lys Arg Val Met Gly Glu Glu Glu
308 1 5 10 15
309 Glu Ser Glu Arg Val Lys Asn Lys Arg Leu Lys Gly Val Glu Glu Glu
310 20 25 30
311 Asp Gly Ser Asp Gly Val Pro Thr Glu Glu Val Glu Glu Phe Phe

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/733,685 DATE: 12/21/2000
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Input Set : A:\seq-list.txt
Output Set: N:\CRF3\12212000\I733685.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:20
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:534 M:283 W: Missing Blank Line separator, <220> field identifier
L:554 M:282 W: Invalid Numeric Header Field, <220> has non-blank data
L:535 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:535 M:283 W: Missing Blank Line separator, <400> field identifier
L:570 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:570 M:283 W: Missing Blank Line separator, <400> field identifier